GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 17:13:47 ; Search time 17398.4 Seconds
(without alignments)
1042.620 Million cell updates/sec

Title: US-09-303-518D-125
Perfect score: 1344
Sequence: 1 atgattaaaatcaaaaaagg.....ccattgagaaggaaggctga 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	107	8.0	349	12	CNS07GYI	AL610380 Anopheles
	2	39	2.9	684	10	BI728886	BI728886 1031102C0
	3	38.8	2.9	686	9	AL628099	AL628099 AL628099
	4	38.6	2.9	497	12	P947R	AL390645 Leishmani
	5	38.2	2.8	455	10	BI956450	BI956450 HVSMEn000
	6	37.8	2.8	437	10	T44736	T44736 7999 Lambda
c	7	37.6	2.8	384	9	AI392198	AI392198 NCSM1D6T3
	8	37.6	2.8	528	10	BG606950	BG606950 WHE2492_E
	9	37.6	2.8	540	10	BF260729	BF260729 HVSMEf002
	10	37.6	2.8	544	10	BF260723	BF260723 HVSMEf002
	11	37.6	2.8	551	10	BF253989	BF253989 HVSMEf000
	12	37.6	2.8	574	10	BF265938	BF265938 HV_CEa001
	13	37.6	2.8	622	10	BI957371	BI957371 HVSMEn000
	14	37.6	2.8	634	10	BI959896	BI959896 HVSMEn002
	15	37.6	2.8	636	10	BI959473	BI959473 HVSMEn001
	16	37.6	2.8	697	10	BF628426	BF628426 HVSMEb000
	17	37.6	2.8	704	10	BF628632	BF628632 HVSMEb000
	18	37.6	2.8	759	10	BF259476	BF259476 HVSMEf001
	19	37.6	2.8	764	10	BF616515	BF616515 HVSMEc001
	20	37.6	2.8	783	10	BF626740	BF626740 HVSMEb000
	21	37.6	2.8	841	10	BF254527	BF254527 HVSMEf000
	22	37.6	2.8	847	10	BI957008	BI957008 HVSMEn000
	23	37.6	2.8	864	10	BI957786	BI957786 HVSMEn001
	24	37.6	2.8	888	9	AW983120	AW983120 HVSMEg000
	25	37.2	2.8	376	10	BF293584	BF293584 WHE2158_E
	26	37.2	2.8	383	10	BF325009	BF325009 su18c01.y
	27	37.2	2.8	893	9	AL523270	AL523270 AL523270
	28	36.8	2.7	481	10	T43876	T43876 7139 Lambda
c	29	36.6	2.7	458	9	AW714071	AW714071 h5f02ne.f
	30	36.4	2.7	617	12	AZ935303	AZ935303 BJ__Ba000
c	31	36.4	2.7	967	12	CNS02UAR	AL214236 Tetraodon
	32	36.2	2.7	328	10	BE424405	BE424405 WHE0078_E
c	33	36.2	2.7	407	9	AW712028	AW712028 f7c01ne.f
	34	36.2	2.7	407	10	BF428970	BF428970 WHE1712_E
	35	36.2	2.7	460	10	BG262553	BG262553 WHE0937_D
	36	36.2	2.7	460	10	BE590713	BE590713 WHE0856_A
c	37	36.2	2.7	505	9	AA614629	AA614629 np54b11.s
	38	36.2	2.7	595	10	BI479848	BI479848 WHE3452_G
	39	36.2	2.7	625	10	BE590921	BE590921 WHE0870_E
	40	36.2	2.7	639	10	BG605187	BG605187 WHE2328_F
	41	36.2	2.7	943	9	AL556080	AL556080 AL556080
	42	36	2.7	489	9	AV939450	AV939450 AV939450
c	43	36	2.7	612	12	AQ161443	AQ161443 mgxb0007D
	44	36	2.7	779	10	BI464724	BI464724 603202344
	45	35.8	2.7	574	10	BI949252	BI949252 HVSME1001
	46	35.8	2.7	621	10	BM490565	BM490565 pgp2n.pk0
	47	35.8	2.7	723	12	AQ858218	AQ858218 nbeb0012O
	48	35.6	2.6	320	9	AV938950	AV938950 AV938950
	49	35.6	2.6	577	9	AV938949	AV938949 AV938949
	50	35.6	2.6	841	10	BG342965	BG342965 HVSMEg000
	51	35.4	2.6	642	9	AA263267	AA263267 LD06355.5
	52	35.2	2.6	458	10	BG322949	BG322949 EM1_13_A1
	53	35.2	2.6	532	10	BG356450	BG356450 EM1_22_F1
	54	35.2	2.6	580	10	BG262171	BG262171 WHE0871_G
	55	35.2	2.6	600	10	BI990516	BI990516 4072-12 M
	56	35.2	2.6	600	10	BI990766	BI990766 4081-21 M
	57	35.2	2.6	619	10	BG464488	BG464488 EM1_70_D0
	58	35.2	2.6	619	10	BE285341	BE285341 601098365
	59	35.2	2.6	661	10	BI960403	BI960403 HVSMEn002
c	60	35.2	2.6	915	12	CNS004JJ	AL078575 Drosophil
	61	35	2.6	285	10	BE425275	BE425275 WHE0311_A
c	62	35	2.6	323	9	AI368671	AI368671 qy61h02.x
c	63	35	2.6	349	9	AW808629	AW808629 MR1-ST011
	64	35	2.6	433	9	AW238848	AW238848 xb29f02.y
c	65	35	2.6	473	9	BB856332	BB856332 BB856332
	66	35	2.6	497	10	BE378302	BE378302 601236326
	67	35	2.6	501	10	BE396602	BE396602 601288849
	68	35	2.6	525	10	BE407307	BE407307 601301064
	69	35	2.6	546	10	W97645	W97645 mf99e09.r1
	70	35	2.6	554	10	BE792826	BE792826 601584823
	71	35	2.6	582	10	BM042302	BM042302 603616381
	72	35	2.6	605	10	BI195835	BI195835 602754956
	73	35	2.6	605	10	BE907017	BE907017 601499836
	74	35	2.6	624	10	BE394122	BE394122 601311607
	75	35	2.6	627	10	BE302953	BE302953 ba71h10.y
	76	35	2.6	636	10	BE255207	BE255207 601115757
	77	35	2.6	650	10	BI064475	BI064475 pgf1n.pk0
	78	35	2.6	659	10	BE254129	BE254129 601113992
	79	35	2.6	666	10	BG299516	BG299516 HVSMEa002
	80	35	2.6	671	10	BE794312	BE794312 601591447
	81	35	2.6	676	10	BM042451	BM042451 603616281
	82	35	2.6	683	10	BM006767	BM006767 603615691
	83	35	2.6	686	10	BG761861	BG761861 602718068
	84	35	2.6	691	10	BG469125	BG469125 602511078
	85	35	2.6	721	10	BE299424	BE299424 601118749
	86	35	2.6	727	10	BE612759	BE612759 601452328
	87	35	2.6	733	10	BG165939	BG165939 602344259
	88	35	2.6	762	10	BI161016	BI161016 602865226
	89	35	2.6	764	10	BG481496	BG481496 602528880
	90	35	2.6	766	9	AL527125	AL527125 AL527125

91	35	2.6	768	9	AL559560	AL559560 AL559560
92	35	2.6	772	10	BG760541	BG760541 602716979
93	35	2.6	775	10	BG397732	BG397732 602438793
94	35	2.6	777	10	BG470987	BG470987 602511964
95	35	2.6	779	9	AL538949	AL538949 AL538949
96	35	2.6	779	10	BG575348	BG575348 602597819
97	35	2.6	779	10	BG756437	BG756437 602715767
98	35	2.6	787	9	AL558662	AL558662 AL558662
99	35	2.6	793	10	BG473919	BG473919 602516384
100	35	2.6	793	10	BG743980	BG743980 602722752

ALIGNMENTS

RESULT 1
CNS07GYI
LOCUS CNS07GYI 349 bp DNA linear GSS 02-OCT-2001
DEFINITION Anopheles gambiae GSS T7 end of clone 23L04 of library NotreDame1 from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
ACCESSION AL610380
VERSION AL610380.1 GI:15916565
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
REFERENCE 1 (bases 1 to 349)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
REFERENCE 2 (bases 1 to 349)
AUTHORS Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
COMMENT This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.
FEATURES Location/Qualifiers
source 1. .349
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="23L04"
/clone_lib="NotreDame1"
/note="end : T7"
BASE COUNT 72 a 100 c 106 g 71 t
ORIGIN

Query Match 8.0%; Score 107; DB 12; Length 349;
Best Local Similarity 58.7%; Pred. No. 3.6e-19;
Matches 185; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

```
Qy    629 atgaattcggcggcccgcatcctgccggtttgagtggcacgcacattcatttcatcgagc 688
          |||| || |  |||||||||||| || ||| ||   || |||||||| |||||| | ||||
Db     32 ATGAGTTTGCTGGCCCGCATCCGGCGGGTCTGGTCGGGACGCACATCCATTTCCTTGAGC 91

Qy    689 cggtcggcgcgaataaaaccgtgtggaccatcaattatcaagatgtaattaccattggcc 748
          ||||  ||  ||  |||   || |||    | |||||||| || ||  ||  |||| ||
Db     92 CGGTGAGCCTGACAAAACAGGTCTGGCATCTTAATTATCAGGACGTCATCGCCATCGGTA 151

Qy    749 gtttgtttgcaacaggccgtctgaacaccgagcgcgtgattgccctaggtggttctcaag 808
            | ||  || | ||    |||  | | || ||| | || ||| | |||||  | || |
Db    152 CGCTCTTCACATCCGGAGAGCTGTGCGCGGAACGCATCATCGCCATCGGTGGGCCGCAGG 211

Qy    809 tcaacaaaccgcgcctcttgcgtaccgttttgggtgcgaaagtatcgcaaattactgcgg 868
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Db    212 CTGCAAACCCGCGTCTGGTGAAGACGCTGATTGGCGCGGATATCAATGAACTGCTGAACG 271

Qy    869 gcgaattggttgacacagacaaccgcgtgatttccggttcggtattgaacggcgcgatta 928
          |||      |     || |||||  ||||||||||||||||  | |  |||  |  |
Db    272 AAGAAACCAAAGCAGGCGAAAACCGGCTGATTTCCGGTTCGGTCCTCAGTGGCCTGCATG 331

Qy    929 cacaaggcgcgcacg 943
          |       |||||||
Db    332 CCGTGCAGGCGCACG 346
```

RESULT 2
BI728886
LOCUS BI728886 684 bp mRNA linear EST 19-SEP-2001
DEFINITION 1031102C06.y1 C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BI728886
VERSION BI728886.1 GI:15704597
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 684)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
JOURNAL Unpublished (2001)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES Location/Qualifiers
source 1. .684
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
BASE COUNT 129 a 248 c 203 g 104 t
ORIGIN

Query Match 2.9%; Score 39; DB 10; Length 684;
Best Local Similarity 51.4%; Pred. No. 5.9;
Matches 90; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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Qy   1092 caacacagccgtcaacggcggcgaccgcgccatggtgccgattggtacttacgagcgcgt 1151
          ||||     |  |||||||| || |  || |||||||  ||   ||  |  | | || | |
Db    196 CAACCACATCCGCAACGGCGACGCCGACGTCATGGTGGCGGGCGGCTCCGAGGCGCCCAT 255
```

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Qy   1152 gatgcccttggatatcctgcccaccctgcttttgcgcgatttaatcgtcggcgataccga 1211
          || ||| |||   |       |  | ||   |  ||||   |   |    || |   |||
Db    256 CATCCCCGTGGGCCTGGGCGGCTTCGTGGCGTGCCGCGCGCTGTCCACGCGCAACGACGA 315

Qy   1212 cagcgcgcaggcattgggttgcttggaattggacgaagaagacctcgctttgtgc 1266
            ||   |||| | | |    | ||| |  |||   || | | |||   || ||
Db    316 TCCCGTCAAGGCCTCGCGCCCTTGGGACTGCGACCGCGACGGCTTCGTGATGGGC 370


RESULT   3
AL628099
LOCUS       AL628099                686 bp    mRNA    linear   EST 02-NOV-2001
DEFINITION  AL628099 XGC-gastrula Silurana tropicalis cDNA clone TGas023g05 5',
            mRNA sequence.
ACCESSION   AL628099
VERSION     AL628099.1  GI:16597582
KEYWORDS    EST.
SOURCE      western clawed frog.
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 686)
  AUTHORS   Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (10_2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Huckle E
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TGas023g05.sp6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES             Location/Qualifiers
     source          1. .686
                     /organism="Silurana tropicalis"
                     /db_xref="taxon:8364"
                     /clone="TGas023g05"
                     /clone_lib="XGC-gastrula"
                     /dev_stage="gastrula (stages 10.5-13 mixed)"
                     /lab_host="Escherichia coli XL1-blue"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from stages
                     10-13 gastrulae.  EcoRI-NotI cut cDNA was then ligated
                     into pCS107 with EcoRI at the 5' end and NotI at the 3'
                     end."
BASE COUNT      188 a    153 c    145 g    199 t      1 others
ORIGIN


  Query Match             2.9%;  Score 38.8;  DB 9;  Length 686;
  Best Local Similarity   57.4%;  Pred. No. 6.8;
  Matches   70;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy    266 cagtcgtgattgccgttgaaggcaacgacgaaatcgagtttgaacgctacgcacctgaag 325
          ||| ||||||  ||| || |||     |    || | |   ||  |  | ||| ||  ||
Db    459 CAGACGTGATGACCGCTGCAGGGTTACATAGTATGGGGAGAGACAGAGAAGCATCTTCAG 518

Qy    326 cgctggcaaacttaagcggcgaagaagtgcgccgcaacctgatccaatccggtttgtgga 385
          |||   | | |  | |    | ||| ||||      ||| ||| |||| |||  ||||| |
Db    519 CGCCAACCAGCCAAGGACACTAAGCAGTGAATACAAACATGAGCCAAACCGCCTTGTGCA 578

Qy    386 ct 387
          ||
Db    579 CT 580


RESULT   4
P947R
LOCUS       P947R                   497 bp    DNA     linear   GSS 25-JUL-2000
DEFINITION  Leishmania major Friedlin PAC P947 right end-sequence, genomic
            survey sequence.
ACCESSION   AL390645
VERSION     AL390645.1  GI:9501621
KEYWORDS    GSS.
SOURCE      Leishmania major.
  ORGANISM  Leishmania major
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Leishmania.
REFERENCE   1  (bases 1 to 497)
  AUTHORS   Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and
            Smith,D.F.
  TITLE     A physical map of the Leishmania major Friedlin genome
  JOURNAL   Genome Res. 8 (2), 135-145 (1998)
  MEDLINE   98146435
REFERENCE   2  (bases 1 to 497)
  AUTHORS   Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and
            Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2000) Leishmania major Friedlin genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            alicat@sanger.ac.uk
COMMENT     see http://www.ebi.ac.uk/parasites/leish.html
            Details of Leishmania sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/L_major/
            The primer sequence can be obtained from alicat@sanger.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .497
                     /organism="Leishmania major"
                     /strain="Friedlin"
                     /db_xref="taxon:5664"
                     /clone="PAC P947"
BASE COUNT       74 a    172 c    145 g    104 t      2 others
ORIGIN


  Query Match             2.9%;  Score 38.6;  DB 12;  Length 497;
  Best Local Similarity   59.6%;  Pred. No. 6.6;
  Matches   65;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy   1172 ccaccctgcttttgcgcgatttaatcgtcggcgataccgacagcgcgcaggcattgggtt 1231
          | || |||||   || ||  ||   || |||||  ||||  |    ||| ||| | | |
Db    231 CGACGCTGCTGCCGCACGCGTTGCGCGCCGGCGCCACCGTCGCGCCGCCGGCCTAGCGCC 290

Qy   1232 gcttggaattggacgaagaagacctcgctttgtgcagcttcgtctgccc 1280
          ||  | ||  | |||||      |||||  | ||   || |||||| |||
Db    291 GCCAGCAACAGAACGAACCCCGTCTCGCATCGTCATGCGTCGTCTTCCC 339


RESULT   5
BI956450
LOCUS       BI956450                455 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEn0003G23f Hordeum vulgare rachis EST library HVcDNA0015
            (normal) Hordeum vulgare cDNA clone HVSMEn0003G23f, mRNA sequence.
ACCESSION   BI956450
VERSION     BI956450.1  GI:16307703
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
            Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
            ,J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex rachis cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
```

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          Tel: 864 656 7288
          Fax: 864 656 4293
          Email: rwing@clemson.edu
          Total hq bases = 327
          Seq primer: AATTAACCCTCACTAAAGGG
          High quality sequence stop: 453.
FEATURES             Location/Qualifiers
     source          1. .455
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEn0003G23f"
                     /clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
                     (normal)"
                     /tissue_type="Rachis"
                     /lab_host="TJC121"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Plants were grown at Washington State University,
                     Pullman, WA in a greenhouse, the rachises were excised and
                     frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close
                     lab at the University of California, Riverside total RNA
                     was prepared, poly(A) was purified, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Chin). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
                     sequence has been trimmed to remove vector sequence and
                     contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT       83 a    150 c    150 g     70 t      2 others
ORIGIN
```

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  Query Match             2.8%;  Score 38.2;  DB 10;  Length 455;
  Best Local Similarity   49.5%;  Pred. No. 8.2;
  Matches   97;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || || | ||||
Db    185 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 244

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db    245 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 304

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
           |  |   ||| ||     ||          || | | | | | | |   ||    |
Db    305 TGAGCTCGTACGCCGGACGGCCGCANGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 364

Qy   1088 agttcaacacagccgt 1103
          ||  ||| |  |||||
Db    365 AGGCCAAGAGCGCCGT 380
```

```
RESULT   6
T44736
LOCUS       T44736                  437 bp    mRNA    linear   EST 07-JAN-1998
DEFINITION  7999 Lambda-PRL2 Arabidopsis thaliana cDNA clone 123P21T7, mRNA
            sequence.
ACCESSION   T44736
VERSION     T44736.1  GI:2759537
KEYWORDS    EST.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 437)
  AUTHORS   Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
            ,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel
            ,E. and Somerville,C.
  TITLE     Genes galore: a summary of methods for accessing results from
            large-scale partial sequencing of anonymous Arabidopsis cDNA clones
  JOURNAL   Plant Physiol. 106, 1241-1255 (1994)
  MEDLINE   95148729
COMMENT     On Jan 7, 1998 this sequence version replaced gi:949002.
            Contact: Thomas Newman
            MSU-DOE Plant Research Laboratory
            Michigan State University
            MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
            Lansing,Mi
            Tel: 517-353-0854
            Fax: 517-353-9168
            Email: 22313tcn@ibm.cl.msu.edu
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .437
                     /organism="Arabidopsis thaliana"
                     /strain="var columbia"
                     /db_xref="taxon:3702"
                     /clone="123P21T7"
                     /clone_lib="Lambda-PRL2"
                     /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
                     Lambda PRL2 is a cDNA library derived from equal
                     quantities of 4 pools of mRNA.  The mRNA sources were 1) 7
                     day germinated etiolated seedlings; 2) tissue culture
                     grown roots; 3) staged plants half with 24 hour light
                     cycle, half on 16 hr light, 8 hour dark- rosettes;  4)
                     same plants as 3 but aerial tissue (stems, flowers and
                     siliques.  The vector is BRL's lambda Zip-Lox.  The cDNA
                     inserts were directionally cloned with Sal-Not arms using
                     oligo dT primed cDNA.  "
BASE COUNT       99 a     87 c    103 g    132 t     16 others
ORIGIN
```

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  Query Match             2.8%;  Score 37.8;  DB 10;  Length 437;
  Best Local Similarity   55.8%;  Pred. No. 10;
  Matches   72;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy    128 tgaaagtcaaggaaggcgatgccgtcaaaaaaggccaagtgctgtttgaagacaaaaaga 187
          | ||||  |   |   |  ||   || ||||||    ||   ||||    |   | |||
Db     71 TCAAAGCTACACAGATCTCTGAAATCGAAAAAGCTTGAGCTGTGTTAATGGCGGAGGAGA 130

Qy    188 atccgggcgtggtgtttactgcgccggcttcaggcaaaatcgccgcgattcaccgtggcg 247
          |   ||  ||| || | || |||| | || ||   || |||||| |||| |   | | |
Db    131 AATGGGTGGTGATGGTGACGGCGCAGACTCCAACGAATATCGCCGTGATTAAGTATTGGG 190

Qy    248 aaaagcgcg 256
          |||| | |
Db    191 GAAAGAGAG 199
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```
RESULT   7
AI392198/c
LOCUS       AI392198                384 bp    mRNA    linear   EST 03-FEB-1999
DEFINITION  NCSM1D6T3 Subtracted Mycelial Neurospora crassa cDNA clone SM1D6 5'
            similar to dolichyl-phosphate-mannose synthase, mRNA sequence.
ACCESSION   AI392198
VERSION     AI392198.1  GI:4220005
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 384)
```

```
  AUTHORS   Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L.,
            Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E.,
            Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K., Miller,R.
            , Ortega,J., Pavlova,I., Perea,J., Todisco,S., Trujillo,R.,
            Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S. and Natvig
            ,D.O.
  TITLE     Expressed sequences from conidial, mycelial, and sexual stages of
            Neurospora crassa
  JOURNAL   Fungal Genet. Biol. 21, 348-363 (1997)
  MEDLINE   97435549
COMMENT     Contact: Natvig,D.O./Nelson,M.A.
            Department of Biology
            University of New Mexico
            Castetter Hall, Albuquerque, NM 87131, USA
            Tel: 505 277 3411
            Fax: 505 277 0304
            Email: ngp@biology.unm.edu.
FEATURES             Location/Qualifiers
     source          1. .384
                     /organism="Neurospora crassa"
                     /strain="74-OR23-IV A (FGSC 2489)"
                     /db_xref="taxon:5141"
                     /clone="SM1D6"
                     /clone_lib="Subtracted Mycelial"
                     /sex="Mating type A"
                     /tissue_type="Mycelium"
                     /dev_stage="Mycelium"
                     /lab_host="E. coli"
                     /note="Vector: pBlueScript SK (-); Site_1: EcoRI; Site_2:
                     XhoI; 2% sucrose for 24 hours.  cDNA directionally cloned
                     into pBluescript  SK(-) using the Uni-ZAP XR vector system
                     (Stratagene, La Jolla,  CA). Previously identified highly
                     expressed clones were subtracted  from this library."
BASE COUNT        90 a    140 c     70 g     73 t     11 others
ORIGIN
```

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  Query Match             2.8%;  Score 37.6;  DB 9;  Length 384;
  Best Local Similarity   47.4%;  Pred. No. 11;
  Matches  100;  Conservative    0;  Mismatches  111;  Indels    0;  Gaps    0;

Qy     717 catcaattatcaagatgtaattaccattggccgtttgtttgcaacaggccgtctgaacac 776
           | || || || | |||||| || || |||||    ||   ||      |      |   |
Db     378 CGTCCATGATGATGATGTAGTTGCCCTTGGCGAACTGGAGGCCGTGAACGTAGGCAGTGC 319

Qy     777 cgagcgcgtgattgccctaggtggttctcaagtcaacaaaccgcgcctcttgcgtaccgt 836
           ||||  || | |||||   |  |||   ||  |  ||     | || |.  || || ||
Db     318 CGAGTCCGAGCTTGCCTGNGCGGGTCTGCAGTTGCACGTGGGGAGCGTAGAGCTTAACGA 259

Qy     837 tttgggtgcgaaagtatcgcaaattactgcgggcgaattggttgacacagacaaccgcgt 896
           ||||  |   |  | | |          | ||| |   | || |||    |. |   |
Db     258 GCTGGGCGGCGACATNTTGGGTGCCGTAGGGGGAGCNGTCGTNGACGATTANGAGTTCCC 199

Qy     897 gatttccggttcggtattgaacggcgcgatt 927
           |    | || | |    || || ||||||
Db     198 AGTCGANGTTTTGCTNGCTAAAGGTGCGATT 168
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```
RESULT   8
BG606950
LOCUS       BG606950                 528 bp    mRNA    linear   EST 17-APR-2001
DEFINITION  WHE2492_E05_I10ZS Triticum monococcum early reproductive apex cDNA
            library Triticum monococcum cDNA clone WHE2492_E05_I10, mRNA
            sequence.
ACCESSION   BG606950
VERSION     BG606950.1  GI:13656933
KEYWORDS    EST.
SOURCE      Triticum monococcum.
  ORGANISM  Triticum monococcum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   Anderson,O.D., Chao,S., Dubcovsky,J., Echenique,V., Han,P.S., Hsia
            ,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L.,
            Stamova,B. and Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Early reproductive apex cDNA library from Triticum
            monococcum
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .528
                     /organism="Triticum monococcum"
                     /cultivar="DV92"
                     /db_xref="taxon:4568"
                     /clone="WHE2492_E05_I10"
                     /clone_lib="Triticum monococcum early reproductive apex
                     cDNA library"
                     /tissue_type="Early reproductive apex"
                     /dev_stage="Seven week-old plants"
                     /lab_host="E. coli XLOLR"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; The tissue, total RNA, and
                     poly(A) RNA were prepared from apex at  double-ridge stage
                     to terminal-spikelet stage during transition from
                     vegetative state to flower state, a cDNA library was made,
                     and the  cDNA clones were in vivo excised at the
                     University of California, Davis  (V. Echenique, B. Stamova
                     , J. Dubcovsky).  Plasmid DNA preparations and  DNA
                     sequencing were performed in the OD Anderson lab (all
                     other authors)."
BASE COUNT        45 a    245 c    140 g     98 t
ORIGIN
```

```
  Query Match             2.8%;  Score 37.6;  DB 10;  Length 528;
  Best Local Similarity   49.5%;  Pred. No. 13;
  Matches   97;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy    1008 cggctgggttgcgccgcagccggacaaatactccatcacgcgtacaaccctcggccattt 1067
           | ||| ||      ||| ||||||||     ||||  | |     |   |||  |||
Db     205 CCGCTCGGCCTTCTCGCGGCCGGACTCCCTCTCCGACGCCACCTCCCGCCTGCGCCGCAA 264

Qy    1068 cctgaaaaacaaactcttcaagttcaacacagccgtcaacggcggcgaccgcgccatggt 1127
           ||| |   ||   | | |||| | || | | | ||||  |  ||     |  ||||  | |
Db     265 CCTCACCTACTTCCGCGTCAACTACACCGCCGTCGTCGCCTTCGCGCTCGCCGCCTCGCT 324

Qy    1128 gccgattggtacttacgagcgcgtgatgcccttggatatcctgcccaccctgcttttgcg 1187
           | |       | | |  || | | || | | |||   ||||  || ||  |   || |
Db     325 CCTGGCCCACCCCTTCTCGCTCCTCATCCTCCTGGGGGTCCTCGCCGCCTGGTGCTTCCT 384

Qy    1188 cgatttaatcgtcggc 1203
           | |  |  ||  || |
Db     385 CTACATCTTCCGCGCC 400
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RESULT   9
BF260729
LOCUS       BF260729                 540 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEf0022M15f Hordeum vulgare seedling root EST library HVcDNA0007
            (Etiolated and unstressed) Hordeum vulgare cDNA clone
            HVSMEf0022M15f, mRNA sequence.
ACCESSION   BF260729
VERSION     BF260729.2  GI:13120922
KEYWORDS    EST.
SOURCE      barley.
```

```
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex unstressed seedling root cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Nov 16, 2000 this sequence version replaced gi:11189842.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 241
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 530.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEf0022M15f"
                     /clone_lib="Hordeum vulgare seedling root EST library
                     HVcDNA0007 (Etiolated and unstressed)"
                     /tissue_type="Seedling root"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedling roots were
                     then harvested, total RNA was prepared, poly(A) RNA was
                     purified, one primary unamplified cDNA library was made,
                     and 1 million pfu were in vivo excised to give pBluescript
                     SK(-) cDNA phagemids. These steps were performed in the TJ
                     Close laboratory at the University of California,
                     Riverside (Choi, Close, Fenton). Phagemids were plated and
                     picked at the Clemson University Genomics Institute (CUGI)
                     (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                     , Rambo, Main). The sequence has been trimmed to remove
                     vector sequence and contains a minimum of 100 bases of
                     phred value 20 or above. For more details on library
                     preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT       111 a    165 c    174 g     90 t
ORIGIN


  Query Match             2.8%;  Score 37.6;  DB 10;  Length 540;
  Best Local Similarity   49.5%;  Pred. No. 13;
  Matches   97;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     167 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 226

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
           ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db     227 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 286

Qy    1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
             |  |   ||| ||     ||           || | | | | | | |  |   ||    |
Db     287 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 346

Qy    1088 agttcaacacagccgt 1103
           ||  |||  |  |||||
Db     347 AGGCCAAGAGCGCCGT 362


RESULT  10
BF260723
LOCUS       BF260723                 544 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEf0022M09f Hordeum vulgare seedling root EST library HVcDNA0007
            (Etiolated and unstressed) Hordeum vulgare cDNA clone
            HVSMEf0022M09f, mRNA sequence.
ACCESSION   BF260723
VERSION     BF260723.2  GI:13120919
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 544)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex unstressed seedling root cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Nov 16, 2000 this sequence version replaced gi:11189836.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 250
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 512.
FEATURES             Location/Qualifiers
     source          1. .544
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEf0022M09f"
                     /clone_lib="Hordeum vulgare seedling root EST library
                     HVcDNA0007 (Etiolated and unstressed)"
                     /tissue_type="Seedling root"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedling roots were
                     then harvested, total RNA was prepared, poly(A) RNA was
                     purified, one primary unamplified cDNA library was made,
                     and 1 million pfu were in vivo excised to give pBluescript
                     SK(-) cDNA phagemids. These steps were performed in the TJ
                     Close laboratory at the University of California,
                     Riverside (Choi, Close, Fenton). Phagemids were plated and
                     picked at the Clemson University Genomics Institute (CUGI)
                     (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                     , Rambo, Main). The sequence has been trimmed to remove
                     vector sequence and contains a minimum of 100 bases of
                     phred value 20 or above. For more details on library
                     preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
```

Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 110 a 165 c 174 g 92 t 3 others
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 544;
Best Local Similarity 49.5%; Pred. No. 13;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

```
Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    167 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 226

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||    | |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db    227 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 286

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
           |  |   ||| ||     ||          || | | | | | | |  |  ||   |
Db    287 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 346

Qy   1088 agttcaacacagccgt 1103
          ||  ||| |  |||||
Db    347 AGGCCAAGAGCGCCGT 362
```

RESULT 11
BF253989
LOCUS BF253989 551 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEf0002L01f Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0002L01f, mRNA sequence.
ACCESSION BF253989
VERSION BF253989.2 GI:13116854
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 551)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library
JOURNAL Unpublished (2001)
COMMENT On Nov 16, 2000 this sequence version replaced gi:11183094.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 300
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 540.
FEATURES Location/Qualifiers
source 1. .551
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEf0002L01f"
/clone_lib="Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates , Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 128 a 151 c 175 g 96 t 1 others
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 551;
Best Local Similarity 49.5%; Pred. No. 13;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
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Db     25 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 84

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||    | |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db     85 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 144

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
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Db    145 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 204

Qy   1088 agttcaacacagccgt 1103
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Db    205 AGGCCAAGAGCGCCGT 220
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RESULT 12
BF265938
LOCUS BF265938 574 bp mRNA linear EST 23-OCT-2001
DEFINITION HV_CEa0013L17f Hordeum vulgare seedling green leaf EST library HVcDNA0004 (Blumeria challenged) Hordeum vulgare cDNA clone HV_CEa0013L17f, mRNA sequence.
ACCESSION BF265938
VERSION BF265938.2 GI:13262431
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 574)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi ,D.W., Fenton,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla13) seedling leaf cDNA library
JOURNAL Unpublished (2001)
COMMENT On Nov 17, 2000 this sequence version replaced gi:11196932.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University

```
          100 Jordan Hall, Clemson, SC 29634, USA
          Tel: 864 656 7288
          Fax: 864 656 4293
          Email: rwing@clemson.edu
          Total hq bases = 348
          Seq primer: AATTAACCCTCACTAAAGGG
          High quality sequence stop: 538.
FEATURES             Location/Qualifiers
     source          1. .574
                     /organism="Hordeum vulgare"
                     /cultivar="CI16155 (Mla13)"
                     /db_xref="taxon:4513"
                     /clone="HV_CEa0013L17f"
                     /clone_lib="Hordeum vulgare seedling green leaf EST
                     library HVcDNA0004 (Blumeria challenged)"
                     /tissue_type="seedling green leaf"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     C.I. 16155 (Mla13) plants were greenhouse grown in the R
                     Wise lab at Iowa State University, Ames, IA; 7 day old
                     green seedlings were challenged with isolate A27 (AvrMla13
                     ) of Blumeria graminis f. sp. hordei, and leaves were
                     harvested 20 and 24 hr post-inoculation and snap frozen;
                     uninoculated leaves were harvested 20 hr post-inoculation
                     (Wei, Wise). In the TJ Close lab at the University of
                     California, Riverside, total RNA was prepared from each
                     sample pool, equal quantities of all three RNA pools were
                     combined, poly(A) RNA was purified from the mixture, one
                     cDNA library was made, and 1 million pfu were in vivo
                     excised to give pBluescript SK(-) cDNA phagemids (Choi,
                     Close). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      119 a    177 c    178 g    100 t
ORIGIN


  Query Match             2.8%;  Score 37.6;  DB 10;  Length 574;
  Best Local Similarity   49.5%;  Pred. No. 13;
  Matches   97;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     178 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 237

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
           ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db     238 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 297

Qy    1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
            |  |   ||| ||     ||          || | | | | | | |  |   ||    |
Db     298 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 357

Qy    1088 agttcaacacagccgt 1103
           ||  ||| |  |||||
Db     358 AGGCCAAGAGCGCCGT 373


RESULT  13
BI957371
LOCUS       BI957371                622 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEn0009D13f Hordeum vulgare rachis EST library HVcDNA0015
            (normal) Hordeum vulgare cDNA clone HVSMEn0009D13f, mRNA sequence.
ACCESSION   BI957371
VERSION     BI957371.1  GI:16308624
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 622)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
            Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
            ,J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex rachis cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 318
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 529.
FEATURES             Location/Qualifiers
     source          1. .622
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEn0009D13f"
                     /clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
                     (normal)"
                     /tissue_type="Rachis"
                     /lab_host="TJC121"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Plants were grown at Washington State University,
                     Pullman, WA in a greenhouse, the rachises were excised and
                     frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close
                     lab at the University of California, Riverside total RNA
                     was prepared, poly(A) was purified, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Chin). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
                     sequence has been trimmed to remove vector sequence and
                     contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      127 a    206 c    183 g    106 t
ORIGIN


  Query Match             2.8%;  Score 37.6;  DB 10;  Length 622;
  Best Local Similarity   49.5%;  Pred. No. 14;
  Matches   97;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     185 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 244

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db    245 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 304

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
          |  |   ||| ||     ||          || | | | | | | |  |   ||     |
Db    305 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 364

Qy   1088 agttcaacacagccgt 1103
          ||  ||| |  |||||
Db    365 AGGCCAAGAGCGCCGT 380
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RESULT 14
BI959896
LOCUS BI959896 634 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEn0022E12f Hordeum vulgare rachis EST library HVcDNA0015 (normal) Hordeum vulgare cDNA clone HVSMEn0022E12f, mRNA sequence.
ACCESSION BI959896
VERSION BI959896.1 GI:16311151
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 634)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons ,J., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 465
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 605.

FEATURES Location/Qualifiers
source 1. .634
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEn0022E12f"
/clone_lib="Hordeum vulgare rachis EST library HVcDNA0015 (normal)"
/tissue_type="Rachis"
/lab_host="TJC121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 131 a 185 c 205 g 113 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 634;
Best Local Similarity 49.5%; Pred. No. 14;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    177 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 236

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db    237 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 296

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
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Db    297 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 356

Qy   1088 agttcaacacagccgt 1103
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Db    357 AGGCCAAGAGCGCCGT 372
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RESULT 15
BI959473
LOCUS BI959473 636 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEn0019N03f Hordeum vulgare rachis EST library HVcDNA0015 (normal) Hordeum vulgare cDNA clone HVSMEn0019N03f, mRNA sequence.
ACCESSION BI959473
VERSION BI959473.1 GI:16310728
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 636)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons ,J., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 585
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 5
High quality sequence stop: 624.

FEATURES Location/Qualifiers
source 1. .636
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEn0019N03f"
/clone_lib="Hordeum vulgare rachis EST library HVcDNA0015 (normal)"
/tissue_type="Rachis"
/lab_host="TJC121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA

was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 132 a 188 c 203 g 113 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 636;
Best Local Similarity 49.5%; Pred. No. 14;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    175 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 234

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db    235 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 294

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
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Db    295 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 354

Qy   1088 agttcaacacagccgt 1103
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Db    355 AGGCCAAGAGCGCCGT 370
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RESULT 16
BF628426
LOCUS BF628426 697 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEb0006A02f Hordeum vulgare seedling shoot EST library HVcDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMEb0006A02f, mRNA sequence.
ACCESSION BF628426
VERSION BF628426.2 GI:13090049
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 697)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex drought-stressed seedling shoot cDNA library
JOURNAL Unpublished (2001)
COMMENT On Dec 19, 2000 this sequence version replaced gi:11892584.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu

Total hq bases = 340
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 681.
FEATURES Location/Qualifiers
source 1. .697
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEb0006A02f"
/clone_lib="Hordeum vulgare seedling shoot EST library HVcDNA0002 (Dehydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 90% RH for 24 hr. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 144 a 206 c 220 g 126 t 1 others
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 697;
Best Local Similarity 49.5%; Pred. No. 15;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    169 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 228

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db    229 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 288

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
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Db    289 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 348

Qy   1088 agttcaacacagccgt 1103
          ||  ||| |  |||||
Db    349 AGGCCAAAAGCGCCGT 364
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RESULT 17
BF628632
LOCUS BF628632 704 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEb0006N12f Hordeum vulgare seedling shoot EST library HVcDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMEb0006N12f, mRNA sequence.
ACCESSION BF628632
VERSION BF628632.2 GI:13090280
KEYWORDS EST.

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SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 704)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex drought-stressed seedling shoot cDNA
            library
  JOURNAL   Unpublished (2001)
COMMENT     On Dec 19, 2000 this sequence version replaced gi:11892790.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 580
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 663.
FEATURES             Location/Qualifiers
     source          1. .704
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEb0006N12f"
                     /clone_lib="Hordeum vulgare seedling shoot EST library
                     HVcDNA0002 (Dehydration stress)"
                     /tissue_type="Seedling shoot"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedlings were
                     incubated at 90% RH for 24 hr. Shoots were then harvested,
                     total RNA was prepared, poly(A) RNA was purified, one
                     primary unamplified cDNA library was made, 600000 pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids.
                     These steps were performed in the TJ Close laboratory at
                     the University of California, Riverside (Choi, Close,
                     Fenton). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      146 a    206 c    226 g    126 t
ORIGIN
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  Query Match             2.8%;  Score 37.6;  DB 10;  Length 704;
  Best Local Similarity   49.5%;  Pred. No. 15;
  Matches   97;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
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Db     164 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 223

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db     224 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 283

Qy    1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
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Db     284 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 343

Qy    1088 agttcaacacagccgt 1103
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Db     344 AGGCCAAGAGCGCCGT 359
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RESULT  18
BF259476
LOCUS       BF259476                759 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEf0019D11f Hordeum vulgare seedling root EST library HVcDNA0007
            (Etiolated and unstressed) Hordeum vulgare cDNA clone
            HVSMEf0019D11f, mRNA sequence.
ACCESSION   BF259476
VERSION     BF259476.2  GI:13119939
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex unstressed seedling root cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Nov 16, 2000 this sequence version replaced gi:11188505.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 469
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 663.
FEATURES             Location/Qualifiers
     source          1. .759
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEf0019D11f"
                     /clone_lib="Hordeum vulgare seedling root EST library
                     HVcDNA0007 (Etiolated and unstressed)"
                     /tissue_type="Seedling root"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedling roots were
                     then harvested, total RNA was prepared, poly(A) RNA was
                     purified, one primary unamplified cDNA library was made,
                     and 1 million pfu were in vivo excised to give pBluescript
                     SK(-) cDNA phagemids. These steps were performed in the TJ
                     Close laboratory at the University of California,
                     Riverside (Choi, Close, Fenton). Phagemids were plated and
                     picked at the Clemson University Genomics Institute (CUGI)
                     (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                     , Rambo, Main). The sequence has been trimmed to remove
                     vector sequence and contains a minimum of 100 bases of
                     phred value 20 or above. For more details on library
                     preparation and sequence analysis see
```

http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 190 a 210 c 230 g 127 t 2 others
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 759;
Best Local Similarity 49.5%; Pred. No. 15;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    ||.| | ||||
Db     32 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 91

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db     92 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 151

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
          |  |   ||| ||     ||          || | | | | | | | |  ||    |
Db    152 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 211

Qy   1088 agttcaacacagccgt 1103
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Db    212 AGGCCAAGAGCGCCGT 227
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RESULT 19
BF616515
LOCUS BF616515 764 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEc0010E03f Hordeum vulgare seedling shoot EST library HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEc0010E03f, mRNA sequence.
ACCESSION BF616515
VERSION BF616515.2 GI:13108021
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 764)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library
JOURNAL Unpublished (2001)
COMMENT On Dec 18, 2000 this sequence version replaced gi:11880249.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 395
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 623.
FEATURES Location/Qualifiers
source 1. .764
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEc0010E03f"
/clone_lib="Hordeum vulgare seedling shoot EST library HVcDNA0003 (Etiolated and unstressed)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates , Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 177 a 217 c 243 g 127 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 764;
Best Local Similarity 49.5%; Pred. No. 15;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
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Db    167 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 226

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db    227 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 286

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
          |  |   ||| ||     ||          || | | | | | | | |  ||    |
Db    287 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 346

Qy   1088 agttcaacacagccgt 1103
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Db    347 AGGCCAAGAGCGCCGT 362
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RESULT 20
BF626740
LOCUS BF626740 783 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEb0001D17f Hordeum vulgare seedling shoot EST library HVcDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMEb0001D17f, mRNA sequence.
ACCESSION BF626740
VERSION BF626740.2 GI:13088174
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 783)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex drought-stressed seedling shoot cDNA library
JOURNAL Unpublished (2001)
COMMENT On Dec 19, 2000 this sequence version replaced gi:11890904.

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 476
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 698.

FEATURES Location/Qualifiers
source 1. .783
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEb0001D17f"
/clone_lib="Hordeum vulgare seedling shoot EST library HVcDNA0002 (Dehydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 90% RH for 24 hr. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 177 a 220 c 252 g 134 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 783;
Best Local Similarity 49.5%; Pred. No. 16;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
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Db    178 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 237

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db    238 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 297

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
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Db    298 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 357

Qy   1088 agttcaacacagccgt 1103
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Db    358 AGGCCAAGAGCGCCGT 373
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RESULT 21
BF254527

LOCUS BF254527 841 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEf0004E12f Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0004E12f, mRNA sequence.
ACCESSION BF254527
VERSION BF254527.2 GI:13117183
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 841)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library
JOURNAL Unpublished (2001)
COMMENT On Nov 16, 2000 this sequence version replaced gi:11183632.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 416
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 580.

FEATURES Location/Qualifiers
source 1. .841
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEf0004E12f"
/clone_lib="Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 192 a 219 c 298 g 132 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 841;
Best Local Similarity 49.5%; Pred. No. 16;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     180 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 239

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db     240 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 299

Qy    1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
            |  |   ||| ||     ||          || | | | | | | |  |   ||    |
Db     300 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 359

Qy    1088 agttcaacacagccgt 1103
           ||  ||| |  |||||
Db     360 AGGCCAAGAGCGCCGT 375
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RESULT 22
BI957008
LOCUS BI957008 847 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEn0006O06f Hordeum vulgare rachis EST library HVcDNA0015 (normal) Hordeum vulgare cDNA clone HVSMEn0006O06f, mRNA sequence.
ACCESSION BI957008
VERSION BI957008.1 GI:16308261
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 847)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons ,J., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 592
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 667.

FEATURES Location/Qualifiers
source 1. .847
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEn0006O06f"
/clone_lib="Hordeum vulgare rachis EST library HVcDNA0015 (normal)"
/tissue_type="Rachis"
/lab_host="TJC121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 183 a 249 c 258 g 157 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 847;
Best Local Similarity 49.5%; Pred. No. 16;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy     908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
           ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db     180 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 239

Qy     968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
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Db     240 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 299

Qy    1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
            |  |   ||| ||     ||          || | | | | | | |  |   ||    |
Db     300 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 359

Qy    1088 agttcaacacagccgt 1103
           ||  ||| |  |||||
Db     360 AGGCCAAGAGCGCCGT 375
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RESULT 23
BI957786
LOCUS BI957786 864 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEn0011F07f Hordeum vulgare rachis EST library HVcDNA0015 (normal) Hordeum vulgare cDNA clone HVSMEn0011F07f, mRNA sequence.
ACCESSION BI957786
VERSION BI957786.1 GI:16309053
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 864)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons ,J., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 458
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 641.

FEATURES Location/Qualifiers
source 1. .864
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEn0011F07f"
/clone_lib="Hordeum vulgare rachis EST library HVcDNA0015 (normal)"
/tissue_type="Rachis"
/lab_host="TJC121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 188 a 221 c 324 g 131 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 864;
Best Local Similarity 49.5%; Pred. No. 16;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    114 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 173

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | |||  ||
Db    174 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 233

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
          |  |   ||| ||     ||          || | | | | | | |   ||    |
Db    234 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 293

Qy   1088 agttcaacacagccgt 1103
          ||  ||| |  |||||
Db    294 AGGCCAAGAGCGCCGT 309
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RESULT 24
AW983120
LOCUS AW983120 888 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEg0008D22f Hordeum vulgare pre-anthesis spike EST library HVcDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone HVSMEg0008D22f, mRNA sequence.
ACCESSION AW983120
VERSION AW983120.3 GI:16317593
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 888)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex pre-anthesis spike cDNA library
JOURNAL Unpublished (2001)
COMMENT On Jun 2, 2000 this sequence version replaced gi:13153638.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 448
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 592.
FEATURES Location/Qualifiers
source 1. .888
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEg0008D22f"
/clone_lib="Hordeum vulgare pre-anthesis spike EST library HVcDNA0008 (white to yellow anther)"
/tissue_type="pre-anthesis spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spike with awns trimmed were collected at white, green and yellow anther stages (Fenton). Total RNA was prepared from each pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close lab (Choi) at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing) Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 195 a 248 c 283 g 162 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 9; Length 888;
Best Local Similarity 49.5%; Pred. No. 17;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||    |     ||| ||| ||   |  |    || | | ||||
Db    166 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 225

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | |||  ||
Db    226 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 285

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
          |  |   ||| ||     ||          || | | | | | | |   ||    |
Db    286 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 345

Qy   1088 agttcaacacagccgt 1103
          ||  ||| |  |||||
Db    346 AGGCCAAGAGCGCCGT 361
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RESULT 25
BF293584
LOCUS BF293584 376 bp mRNA linear EST 17-NOV-2000
DEFINITION WHE2158_E09_J18ZS Triticum turgidum L. var. durum (durum wheat) whole plant cDNA library Triticum turgidum cDNA clone WHE2158_E09_J18, mRNA sequence.
ACCESSION BF293584

```
VERSION     BF293584.1  GI:11224648
KEYWORDS    EST.
SOURCE      Triticum turgidum.
  ORGANISM  Triticum turgidum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Close,T.J.,
            Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Kianian,P., Lazo,G.R.,
            Miller,R., Otto,C., Rausch,C.J., Seaton,C.L., Simons,K., Tong,J.C.
            and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Whole plant cDNA library from Triticum turgidum L. var.
            durum
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Triticum turgidum"
                     /cultivar="Langdon-16"
                     /db_xref="taxon:4571"
                     /clone="WHE2158_E09_J18"
                     /clone_lib="Triticum turgidum L. var. durum (durum wheat)
                     whole plant cDNA library"
                     /tissue_type="All tissues"
                     /dev_stage="Different growth stages"
                     /lab_host="E. coli SOLR"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Plants were grown in a growth
                     chamber at North Dakota State University (Kianian, Otto,
                     Simons). Tissues collected from seven-day etiolated
                     seedling leaf, stem, root and seed; leaf from plant at
                     fourth leaf stage; spike from pre-anthesis through 20
                     days after anthesis; flag leaf; leaf and stem tissue from
                     tillers. and root. Total RNA and poly(A) RNA were
                     prepared from each tissue and then pooled, a cDNA library
                     was made, and the cDNA clones were in vivo excised to give
                     pBluescript phagemids in the TJ Close lab (Akhunov, Chin,
                     Choi, Close, Fenton, Kianian, Otto, Simons, Zhang) at the
                     University of California, Riverside. Plasmid DNA
                     preparations and DNA sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT       37 a    154 c    136 g    49 t
ORIGIN

  Query Match             2.8%;  Score 37.2;  DB 10;  Length 376;
  Best Local Similarity   55.4%;  Pred. No. 14;
  Matches   72;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy    1197 cgtcggcgataccgacagcgcgcaggcattgggttgcttggaattggacgaagaagacct 1256
           || || |||  |||    || | |||     |   ||| |||  ||| ||  || ||| |
Db      57 CGGCGCCGAGGCCGGGGCCGGGGAGGTGCCGCTGAGCTGGGAGCTGGGCGTGGAGGACGT 116

Qy    1257 cgctttgtgcagcttcgtctgcccgggcaaatacgaatacggcccgctgttgcgcaaagt 1316
           |||      | | |||| || | |||||     ||   |||   || ||  |||    ||
Db     117 CGCCGACGACGGGTTCGGCTTCGCGGGCGCCGGCGGCGACGAGGCGGTGGCGCGGCGCGT 176

Qy    1317 gctggaaacc 1326
           |||| | | |
Db     177 GCTGCAGAGC 186
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```
RESULT  26
BF325009
LOCUS       BF325009                383 bp    mRNA    linear   EST 06-DEC-2001
DEFINITION  su18c01.y1 Gm-c1066 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1066-2017 5' similar to TR:Q9SDA7 Q9SDA7 AT2G17030 PROTEIN. ;;
            mRNA sequence.
ACCESSION   BF325009
VERSION     BF325009.1  GI:11274672
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 383)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Insert Length: 1093   Std Error: 0.00
            High quality sequence stop: 382.
FEATURES             Location/Qualifiers
     source          1. .383
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1066-2017"
                     /clone_lib="Gm-c1066"
                     /tissue_type="Leaf and shoot tip, salt stressed, 2 week
                     old seedling"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from mRNA isolated
                     from unexpanded leaves and the shoot tips of 2 week old
                     seedling from the cultivar Williams. The 2 week old
                     seedlings were salt stressed in a solution of 500mM NaCl
                     for 3 days prior to harvesting. Complementary DNA was
                     synthesized from mRNA using a primer consisting of a
                     poly(dT) sequence with a XhoI restriction site. EcoRI
                     adapters were ligated to the blunt-ended cDNA fragments
                     followed by XhoI digestion. The cDNA fragments were
                     directionally cloned into the EcoRI-XhoI restriction site
                     of the pBluescript vector. The ligated cDNA fragments were
                     transformed into DH10B host cells (GibcoBRL). This library
                     was constructed in the laboratory of Dr. Randy
                     Shoemaker."
BASE COUNT       75 a     91 c    137 g     79 t      1 others
ORIGIN

  Query Match             2.8%;  Score 37.2;  DB 10;  Length 383;
  Best Local Similarity   48.6%;  Pred. No. 14;
  Matches  102;  Conservative    0;  Mismatches  108;  Indels    0;  Gaps    0;

Qy    1083 cttcaagttcaacacagccgtcaacggcggcgaccgcgccatggtgccgattggtactta 1142
           | ||| | |     | |  | |   |||  |  || ||||   | |||  |   |  |
Db      52 CGTCAGGGTGCGGCCGGATGACGGTGGCCTCACCCTCGCCGCCGAGCCTGTCTTTGGTGG 111

Qy    1143 cgagcgcgtgatgcccttggatatcctgcccaccctgcttttgcgcgatttaatcgtcgg 1202
```

```
Db     112 CGACAAGAAGTTCCTCGTGGAGTCCGAGGGCGCGCTGCTGCTCGTCGACATGTACCTCTC 171

Qy    1203 cgataccgacagcgcgcaggcattgggttgcttggaattggacgaagaagacctcgcttt 1262
Db     172 CTACTACTCCTGCACGCAGGGTTTGTTCCACGAGGATTTCGACGAGGAAGATGTGGCCGG 231

Qy    1263 gtgcagcttcgtctgcccgggcaaatacga 1292
Db     232 GATGGGGTGGGAGAGGACGGTGAAGTTTGA 261


RESULT  27
AL523270
LOCUS       AL523270                893 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL523270 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC001YH12 5
            prime, mRNA sequence.
ACCESSION   AL523270
VERSION     AL523270.1  GI:12786763
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 893)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .893
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DC001YH12"
                     /clone_lib="LTI_NFL003_NBC3"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      168 a    282 c    285 g    153 t      5 others
ORIGIN


  Query Match             2.8%;  Score 37.2;  DB 9;  Length 893;
  Best Local Similarity   54.8%;  Pred. No. 22;
  Matches   69;  Conservative    2;  Mismatches   55;  Indels    0;  Gaps    0;

Qy    1215 cgcgcaggcattgggttgcttggaattggacgaagaagacctcgctttgtgcagcttcgt 1274
Db     258 CGGGGCTGCAACCGCCAGCKCCTCAGGGGCCGCCGAGGATGGGGCCTGCKGCTGCCTGCC 317

Qy    1275 ctgcccgggcaaatacgaatacggcccgctgttgcgcaaagtgctggaaaccattgagaa 1334
Db     318 CAACCCGGGCACATTCGAGGAGTGCCACCGGAAGTGCAAGGAGCTGTTTCCCATTCAGAT 377

Qy    1335 ggaagg 1340
Db     378 GGAGGG 383


RESULT  28
T43876
LOCUS       T43876                  481 bp    mRNA    linear   EST 07-JAN-1998
DEFINITION  7139 Lambda-PRL2 Arabidopsis thaliana cDNA clone 118M9T7, mRNA
            sequence.
ACCESSION   T43876
VERSION     T43876.1  GI:948248
KEYWORDS    EST.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 481)
  AUTHORS   Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
            ,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel
            ,E. and Somerville,C.
  TITLE     Genes galore: a summary of methods for accessing results from
            large-scale partial sequencing of anonymous Arabidopsis cDNA clones
  JOURNAL   Plant Physiol. 106, 1241-1255 (1994)
  MEDLINE   95148729
COMMENT     On Nov 29, 1993 this sequence version replaced gi:636464.
            Contact: Thomas Newman
            MSU-DOE Plant Research Laboratory
            Michigan State University
            MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
            Lansing,Mi
            Tel: 517-353-0854
            Fax: 517-353-9168
            Email: 22313tcn@ibm.cl.msu.edu
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .481
                     /organism="Arabidopsis thaliana"
                     /strain="var columbia"
                     /db_xref="taxon:3702"
                     /clone="118M9T7"
                     /clone_lib="Lambda-PRL2"
                     /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
                     Lambda PRL2 is a cDNA library derived from equal
                     quantities of 4 pools of mRNA.  The mRNA sources were 1) 7
                     day germinated etiolated seedlings; 2) tissue culture
                     grown roots; 3) staged plants half with 24 hour light
                     cycle, half on 16 hr light, 8 hour dark- rosettes;  4)
                     same plants as 3 but aerial tissue (stems, flowers and
                     siliques.  The vector is BRL's lambda Zip-Lox.  The cDNA
                     inserts were directionally cloned with Sal-Not arms using
                     oligo dT primed cDNA.  "
BASE COUNT      122 a     96 c    113 g    133 t     17 others
ORIGIN


  Query Match             2.7%;  Score 36.8;  DB 10;  Length 481;
  Best Local Similarity   55.0%;  Pred. No. 21;
  Matches   71;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy     128 tgaaagtcaaggaaggcgatgccgtcaaaaaaggccaagtgctgtttgaagacaaaaaga 187
Db      47 TCAAAGCTACACAGATCTCTGGAATCGAAAAAGCTTGANCTGTGTTAATGGCGGAGGAGA 106

Qy     188 atccgggcgtggtgtttactgcgccggcttcaggcaaaatcgccgcgattcaccgtggcg 247
Db     107 AATGGGTGGTGATGGTGACGGCGCAGACTCCAACGAATATCGCCGTGATTAAGTATTGGG 166

Qy     248 aaaagcgcg 256
Db     167 GAAAGAGAG 175


RESULT  29
AW714071/c
LOCUS       AW714071                458 bp    mRNA    linear   EST 25-APR-2000
DEFINITION  h5f02ne.f1 Neurospora crassa evening cDNA library Neurospora crassa
            cDNA clone h5f02ne 5', mRNA sequence.
```

```
ACCESSION   AW714071
VERSION     AW714071.1  GI:7603237
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 458)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: h5f02ne.r1
            Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 345.
FEATURES             Location/Qualifiers
     source          1. .458
                     /organism="Neurospora crassa"
                     /strain="Strain 30-7 (bd; A)"
                     /db_xref="taxon:5141"
                     /clone="h5f02ne"
                     /clone_lib="Neurospora crassa evening cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
                     EcoRI; See: Bell-Perdersen,D., et al. PNAS 93:13096,1996.
                     5' end of cDNA cloned into XbaI site of pBluescript; 3'
                     end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT      110 a    171 c     85 g     92 t
ORIGIN
```

```
  Query Match              2.7%;  Score 36.6;  DB 9;  Length 458;
  Best Local Similarity   48.3%;  Pred. No. 23;
  Matches  102;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy     717 catcaattatcaagatgtaattaccattggccgtttgtttgcaacaggccgtctgaacac 776
           | || || || | |||||| || || |||||    ||   ||    | |       |  |
Db     408 CGTCCATGATGATGATGTAGTTGCCCTTGGCGAACTGGAGGCCGTGGACGTAGGCAGTGC 349

Qy     777 cgagcgcgtgattgccctaggtggttctcaagtcaacaaaccgcgcctcttgcgtaccgt 836
           ||||  || | ||||||   |  |||   ||  |  ||     | || |   || || ||
Db     348 CGAGTCCGAGCTTGCCTGTGCGGGTCTGCAGTTGCACGTGGGGAGCGTAGAGCTTAACGA 289

Qy     837 tttgggtgcgaaagtatcgcaaattactgcgggcgaattggttgacacagacaaccgcgt 896
             |||| |   |  | | |         | ||| |   | || |||    || | |  |
Db     288 GCTGGGCGGCGACATCTTGGGTGCCGTCGGGGGAGCCGTCGTCGACGATTACGAGTTCCC 229

Qy     897 gatttccggttcggtattgaacggcgcgatt 927
             |    | || | |    || || ||||||
Db     228 AGTCGATGTTTTGCTCGCTAAAGGTGCGATT 198
```

```
RESULT  30
AZ935303
LOCUS       AZ935303                617 bp    DNA     linear   GSS 24-APR-2001
DEFINITION  BJ__Ba0003J23f B. japonicum BAC library Bradyrhizobium japonicum
            genomic, DNA sequence.
ACCESSION   AZ935303
VERSION     AZ935303.1  GI:13777815
KEYWORDS    GSS.
SOURCE      Bradyrhizobium japonicum.
  ORGANISM  Bradyrhizobium japonicum
            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
            Bradyrhizobium group; Bradyrhizobium.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A., Goicoechea
            ,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.
  TITLE     A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
            genome
  JOURNAL   Genome Res. 11 (8), 1434-1440 (2001)
  MEDLINE   21376150
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Class: BAC ends
            High quality sequence stop: 560.
FEATURES             Location/Qualifiers
     source          1. .617
                     /organism="Bradyrhizobium japonicum"
                     /strain="USDA110"
                     /db_xref="taxon:375"
                     /clone_lib="B. japonicum BAC library"
                     /lab_host="E. coli"
                     /note="Vector: pIndigo536; Site_1: HindIII"
BASE COUNT      108 a    193 c    216 g     98 t      2 others
ORIGIN
```

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  Query Match              2.7%;  Score 36.4;  DB 12;  Length 617;
  Best Local Similarity   47.9%;  Pred. No. 30;
  Matches  103;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy    1101 cgtcaacggcggcgaccgcgccatggtgccgattggtacttacgagcgcgtgatgccctt 1160
           | |||    ||||||| || |||| | | ||   |       |  |   | |  | |  |
Db     328 CATCATGACCGGCGACGGCACCATCGCGACGGCGGTCGAGGCCATGAAGGCGGGGGCGCT 387

Qy    1161 ggatatcctgcccaccctgcttttgcgcgatttaatcgtcggcgataccgacagcgcgca 1220
           ||   | | | ||  | | |   || |    |  || |  ||     ||  ||||||
Db     388 CGACTACATTCTCAAGCCGTTCAAGCTCAGCGTCGTCATTCCCGTGCTGGAGCGCGCGCT 447

Qy    1221 ggcattgggttgcttggaattggacgaagaagacctcgctttgtgcagcttcgtctgccc 1280
           ||  || |  || || |  ||||  | |  || || ||  || |   |  ||   | |
Db     448 CGCGGTGCGGCGCCTGCACCTGGAGAATGCNGAGCTGGCGCTGCGGGTCCGCGAGCGGAC 507

Qy    1281 gggcaaatacgaatacggcccgctgttgcgcaaag 1315
             | |   ||||  || | | | |  || | | |
Db     508 CCTCGAGCTCGAAGCCGCCACCCGGGAGCTCGAGG 542
```

```
RESULT  31
CNS02UAR/c
LOCUS       CNS02UAR                967 bp    DNA     linear   GSS 15-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            166L18 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL214236
VERSION     AL214236.1  GI:7873055
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 967)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 967)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
```

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            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 967)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .967
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="166L18"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG166DF09SP1-end :
                     PUC-Ori"
BASE COUNT      249 a    230 c    219 g    266 t      3 others
ORIGIN


  Query Match             2.7%;  Score 36.4;  DB 12;  Length 967;
  Best Local Similarity   53.7%;  Pred. No. 37;
  Matches   73;  Conservative    1;  Mismatches   62;  Indels    0;  Gaps    0;

Qy     455 atgcgatggacaccaatccgctggctgccgaccctacggtcattatcaaagaagccgccg 514
           ||||||    |  || :|| |||| ||     ||  ||  | |||  | ||    || || |
Db     963 ATGCGAAACAGCCCGRTCTGCTGACTTGTCACAATAAAGGCATGTTGAAGTGGGCGGCAG 904

Qy     515 aggatttcaaacgcggcctgttggtattgagccgtttgaccgaacgcaaaatccatgttt 574
           ||||    | |  |  | ||||  |  ||  |   ||| | |  |   |||   ||||
Db     903 AGGAACAAACAAACACCGTGTTTTTCCTGCCCACCTTGGCAGCGCTGGAAAAAAATGTGG 844

Qy     575 gtaaggcagctggcgc 590
           ||||  |||| | ||
Db     843 TTAAGTAAGCTTGGGC 828


RESULT  32
BE424405
LOCUS       BE424405                328 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  WHE0078_E09_J18ZS Wheat endosperm cDNA library Triticum aestivum
            cDNA clone WHE0078_E09_J18, mRNA sequence.
ACCESSION   BE424405
VERSION     BE424405.1  GI:9422248
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 328)
  AUTHORS   Altenbach,S., Anderson,O.D., Chao,S., Galili,G., Han,P.S., Hsia
            ,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and
            Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Endosperm cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .328
                     /organism="Triticum aestivum"
                     /cultivar="Cheyenne"
                     /db_xref="taxon:4565"
                     /clone="WHE0078_E09_J18"
                     /clone_lib="Wheat endosperm cDNA library"
                     /tissue_type="Endosperm"
                     /dev_stage="5 to 30 days post anthesis seed"
                     /lab_host="E. coli SOLR"
                     /note="Vector: Lambda ZAP II, excised phagemid; Site_1:
                     EcoRI; Seeds collected, endosperm isolated, and RNA
                     prepared by Susan  Altenbach. Library constructed by
                     Stratagene, Inc. Plasmid DNA  preparations and DNA
                     sequencing were performed in the OD Anderson lab."
BASE COUNT      96 a     83 c     83 g     66 t
ORIGIN


  Query Match             2.7%;  Score 36.2;  DB 10;  Length 328;
  Best Local Similarity   50.3%;  Pred. No. 26;
  Matches   89;  Conservative    0;  Mismatches   88;  Indels    0;  Gaps    0;

Qy     152 tcaaaaaaggccaagtgctgtttgaagacaaaaagaatccgggcgtggtgtttactgcgc 211
           ||||  | ||  |    | | || || ||   ||| ||       | |||     || | ||
Db      62 TCAAGCATGGTGACAAGATCTTGGACGAAGCAAACAAGGTCTTCTTGGGACACACAGTGC 121

Qy     212 cggcttcaggcaaaatcgccgcgattcaccgtggcgaaaagcgcgtacttcagtcagtcg 271
           ||  ||||||| | |  |||||| |  |  | |||     |   ||  ||| ||
Db     122 AACTGGCAATCAAAATCTCTGGCATTCACTGGTGGTACAAGGTTCCAAGCCATGCAGCCG 181

Qy     272 tgattgccgttgaaggcaacgacgaaatcgagtttgaacgctacgcacctgaagcgc 328
           | |  | | ||     | || ||  |    ||    ||  |||||  |||   ||| |
Db     182 AGGTCACAGCTGGGTACTACAACTTACATGATAGAGACGGCTACAGACCCATAGCAC 238


RESULT  33
AW712028/c
LOCUS       AW712028                407 bp    mRNA    linear   EST 25-APR-2000
DEFINITION  f7c01ne.f2 Neurospora crassa evening cDNA library Neurospora crassa
            cDNA clone f7c01ne 5', mRNA sequence.
ACCESSION   AW712028
VERSION     AW712028.1  GI:7601100
KEYWORDS    EST.
SOURCE      Neurospora crassa.
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 407)
  AUTHORS   Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
  TITLE     Two Neurospora crassa EST Databases
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: f7c01ne.r1
            Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 263.
FEATURES             Location/Qualifiers
     source          1. .407
                     /organism="Neurospora crassa"
                     /strain="Strain 30-7 (bd; A)"
                     /db_xref="taxon:5141"
                     /clone="f7c01ne"
                     /clone_lib="Neurospora crassa evening cDNA library"
                     /tissue_type="tissue harvested following 22hr growth in
                     dark"
                     /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
```

EcoRI; See: Bell-Perdersen,D., et al. PNAS 93:13096,1996. 5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT 97 a 150 c 76 g 84 t
ORIGIN

Query Match 2.7%; Score 36.2; DB 9; Length 407;
Best Local Similarity 48.3%; Pred. No. 28;
Matches 101; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

```
Qy    719 tcaattatcaagatgtaattaccattggccgtttgtttgcaacaggccgtctgaacaccg 778
          || || || | |||||| || || ||||||    ||   ||    | |      |   |||
Db    406 TCCATGATGATGATGTAGTTGCCCTTGGCGAACTGGAGGCCGTGGACGTAGGCAGTGCCG 347

Qy    779 agcgcgtgattgccctaggtggttctcaagtcaacaaaccgcgcctcttgcgtaccgttt 838
          ||  || | |||||   |  |||   ||  |  ||     | || |   || || ||
Db    346 AGTCCGAGCTTGCCTGTGCGGGTCTGCAGTTGCACGTGGGGAGCGTAGAGCTTAACGAGC 287

Qy    839 tgggtgcgaaagtatcgcaaattactgcgggcgaattggttgacacagacaaccgcgtga 898
          ||||  |   |  | | |         | ||| |   | || |||    || |   |
Db    286 TGGGCGGCGACATCTTGGGTGCCGTCGGGGGAGCCGTCGTCGACGATTACGAGTTCCCAG 227

Qy    899 tttccggttcggtattgaacggcgcgatt 927
          |    | || | |    || || ||||||
Db    226 TCGATGTTTTGCTCGCTAAAGGTGCGATT 198
```

RESULT 34
BF428970
LOCUS BF428970 407 bp mRNA linear EST 29-NOV-2000
DEFINITION WHE1712_E10_J20ZS Wheat heat stressed spike cDNA library Triticum aestivum cDNA clone WHE1712_E10_J20, mRNA sequence.
ACCESSION BF428970
VERSION BF428970.1 GI:11440887
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 407)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Malatrasi,M., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat genomes - Heat stressed spike cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1. .407
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1712_E10_J20"
/clone_lib="Wheat heat stressed spike cDNA library"
/tissue_type="Whole spike"
/dev_stage="Spikes at 5, 10, 15 and 20 days after anthesis"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Spikes at 5, 10, 15 and 20 days after anthesis were heat stressed under two conditions at Texas Tech University (D. Zhang in HT Nguyrn lab): (1) at 38 C for 4 hours and (2) 5 days of cyclic treatment of 38 C for 4 hours. Total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton, Malatrasi) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT 124 a 94 c 112 g 77 t
ORIGIN

Query Match 2.7%; Score 36.2; DB 10; Length 407;
Best Local Similarity 50.3%; Pred. No. 28;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

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Qy    152 tcaaaaaaggccaagtgctgtttgaagacaaaaagaatccgggcgtggtgtttactgcgc 211
          ||||  | ||  |   | | || || ||   ||| ||      | |||  |  |  | ||
Db     81 TCAAGCACGGTGACAAGATCTTGGACGAAGCAAACAAGGTCTTCTTGGGATGCAGGGTGC 140

Qy    212 cggcttcaggcaaaatcgccgcgattcaccgtggcgaaaagcgcgtacttcagtcagtcg 271
          |    ||| |||||||| | |  |||||| |  |  | | |      |   ||  ||| ||
Db    141 AGCTGGCAGTCAAAATCTCTGGCATTCACTGGTGGTACAGGGTTCCAAACCATGCAGCCG 200

Qy    272 tgattgccgttgaaggcaacgacgaaatcgagtttgaacgctacgcacctgaagcgc 328
          | |  | | ||    | || ||  |   ||    ||  |||||  | |   ||| |
Db    201 AGCTCACAGCTGGGTACTACAACTTAGATGACAGAGACGGCTACAGAACCATAGCAC 257
```

RESULT 35
BG262553
LOCUS BG262553 460 bp mRNA linear EST 16-FEB-2001
DEFINITION WHE0937_D10_G19ZS Wheat 5-15 DAP spike cDNA library Triticum aestivum cDNA clone WHE0937_D10_G19, mRNA sequence.
ACCESSION BG262553
VERSION BG262553.1 GI:12863829
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 460)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
TITLE The structure and function of the expressed portion of the wheat genomes - 5-15 DAP spike cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1. .460
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0937_D10_G19"
/clone_lib="Wheat 5-15 DAP spike cDNA library"
/tissue_type="Spike"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Spikes at 5, 10 and 15 DAP were harvested, total RNA and poly(A) RNA were prepared, a cDNA library

was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 131 a 117 c 118 g 94 t
ORIGIN

Query Match 2.7%; Score 36.2; DB 10; Length 460;
Best Local Similarity 50.3%; Pred. No. 30;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

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Qy    152 tcaaaaaaggccaagtgctgtttgaagacaaaaagaatccgggcgtggtgtttactgcgc 211
          ||||  | ||  |   | | || || ||   ||| ||      | |||     || | ||
Db    191 TCAAGCATGGTGACAAGATCTTGGACGAAGCAAACAAGGTCTTCTTGGGACACACAGTGC 250

Qy    212 cggcttcaggcaaaatcgccgcgattcaccgtggcgaaaagcgcgtacttcagtcagtcg 271
              ||  ||||||| | |  |||||| |  |  | |||     |   ||  ||| ||
Db    251 AACTGGCAATCAAAATCTCTGGCATTCACTGGTGGTACAAGGTTCCAAGCCATGCAGCCG 310

Qy    272 tgattgccgttgaaggcaacgacgaaatcgagtttgaacgctacgcacctgaagcgc 328
            | |  | | ||    | || ||  |   ||   ||  |||||  |||   ||| |
Db    311 AGGTCACAGCTGGGTACTACAACTTACATGATAGAGACGGCTACAGACCCATAGCAC 367
```

RESULT 36
BE590713
LOCUS BE590713 460 bp mRNA linear EST 18-AUG-2000
DEFINITION WHE0856_A07_A14ZS Wheat 20-45 DAP spike cDNA library.Triticum aestivum cDNA clone WHE0856_A07_A14, mRNA sequence.
ACCESSION BE590713
VERSION BE590713.1 GI:9845786
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 460)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
TITLE The structure and function of the expressed portion of the wheat genomes - 20-45 DAP spike cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1. .460
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0856_A07_A14"
/clone_lib="Wheat 20-45 DAP spike cDNA library"
/tissue_type="Spike and seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 129 a 117 c 114 g 100 t
ORIGIN

Query Match 2.7%; Score 36.2; DB 10; Length 460;
Best Local Similarity 50.3%; Pred. No. 30;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

```
Qy    152 tcaaaaaaggccaagtgctgtttgaagacaaaaagaatccgggcgtggtgtttactgcgc 211
          ||||  | ||  |   | | || || ||   ||| ||      | |||     || | ||
Db    227 TCAAGCATGGTGACAAGATCTTGGACGAAGCAAACAAGGTCTTCTTGGGACACACAGTGC 286

Qy    212 cggcttcaggcaaaatcgccgcgattcaccgtggcgaaaagcgcgtacttcagtcagtcg 271
              ||  ||||||| | |  |||||| |  |  | |||     |   ||  ||| ||
Db    287 AACTGGCAATCAAAATCTCTGGCATTCACTGGTGGTACAAGGTTCCAAGCCATGCAGCCG 346

Qy    272 tgattgccgttgaaggcaacgacgaaatcgagtttgaacgctacgcacctgaagcgc 328
            | |  | | ||    | || ||  |   ||   ||  |||||  |||   ||| |
Db    347 AGGTCACAGCTGGGTACTACAACTTACATGATAGAGACGGCTACAGACCCATAGCAC 403
```

RESULT 37
AA614629/c
LOCUS AA614629 505 bp mRNA linear EST 16-OCT-1997
DEFINITION np54b11.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1130109 3' similar to gb:J04456 GALECTIN-1 (HUMAN);, mRNA sequence.
ACCESSION AA614629
VERSION AA614629.1 GI:2466825
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 505)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 549 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 388.
FEATURES Location/Qualifiers
source 1. .505
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1130109"
/clone_lib="NCI_CGAP_Br1.1"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. (The normalized version of this library is NCI_CGAP_Br2.) Library was constructed by Bento Soares and M. Fatima Bonaldo. "

```
BASE COUNT       93 a    130 c    176 g    106 t
ORIGIN

  Query Match             2.7%;  Score 36.2;  DB 9;  Length 505;
  Best Local Similarity   55.0%;  Pred. No. 31;
  Matches   71;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy     398 cccgtccgttcagcaaaattcctgccgtcgatgccgagccgttcgccatcttcgtcaatg 457
           ||   | |  |  |||  | || | || | | |       |||| ||| |  | ||||
Db     174 CCAACCTGACCGTCAAGCTGCCAGACGGCTACGAATTCAAGTTCCCCAACCGCCTCAACC 115

Qy     458 cgatggacaccaatccgctggctgccgaccctacggtcattatcaaagaagccgccgagg 517
           |  || ||||||    ||||| || ||| ||    |||  ||||||   | ||||   |
Db     114 TGGAGGCCACCAACTACCTGGCAGCTGACGCTGACTTCACGATCAAACGTGTCGCCCTTG 55

Qy     518 atttcaaac 526
           | |  || |
Db      54 ACTGAAATC 46


RESULT  38
BI479848
LOCUS       BI479848                595 bp    mRNA    linear   EST 27-AUG-2001
DEFINITION  WHE3452_G11_M22ZS Wheat pre-anthesis spike cDNA library Triticum
            aestivum cDNA clone WHE3452_G11_M22, mRNA sequence.
ACCESSION   BI479848
VERSION     BI479848.1  GI:15315438
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
            Seaton,C.L. and Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Pre-anthesis spike cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE3452_G11_M22"
                     /clone_lib="Wheat pre-anthesis spike cDNA library"
                     /tissue_type="Spike before anthesis"
                     /dev_stage="Adult plant"
                     /lab_host="E. coli SOLR"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
                     greenhouse.  Whole spike with awns trimmed,  white, green
                     and yellow anther were collected and total RNA, and
                     poly(A) RNA were prepared, a cDNA library was made, and
                     the cDNA  clones were in vivo excised to give pBluescript
                     phagemids in the TJ  Close lab (Choi, Close, Fenton) at
                     the University of California,  Riverside.  Plasmid DNA
                     preparations and DNA sequencing were performed  in the OD
                     Anderson lab (all other authors)."
BASE COUNT      167 a    151 c    145 g    131 t      1 others
ORIGIN


  Query Match             2.7%;  Score 36.2;  DB 10;  Length 595;
  Best Local Similarity   50.3%;  Pred. No. 34;
  Matches   89;  Conservative    0;  Mismatches   88;  Indels    0;  Gaps    0;

Qy     152 tcaaaaaaggccaagtgctgtttgaagacaaaaagaatccgggcgtggtgtttactgcgc 211
           ||||  | ||  |   | | || || ||   ||| ||      | |||     |  | ||
Db      33 TCAAGCACGGTGACAAGATCTTGGACGAAGCAAACAAGGTCTTCTTGGGACACAGAGTGC 92

Qy     212 cggcttcaggcaaaatcgccgcgattcaccgtggcgaaaagcgcgtacttcagtcagtcg 271
           ||  ||||||| | |  |||||| |  |  | |||     |   ||  ||| ||
Db      93 AACTGGCAATCAAAATCTCTGGCATTCACTGGTGGTACAAGGTTCCAAGCCATGCAGCCG 152

Qy     272 tgattgccgttgaaggcaacgacgaaatcgagtttgaacgctacgcacctgaagcgc 328
           |||  | | ||    | || ||  |   ||    ||  |||||  |||   ||| |
Db     153 AGATCACAGCTGGGTACTACAACTTACATGATAGAGATGGCTACAGACCCATAGCAC 209


RESULT  39
BE590921
LOCUS       BE590921                625 bp    mRNA    linear   EST 18-AUG-2000
DEFINITION  WHE0870_E02_J04ZS Wheat 20-45 DAP spike cDNA library Triticum
            aestivum cDNA clone WHE0870_E02_J04, mRNA sequence.
ACCESSION   BE590921
VERSION     BE590921.1  GI:9845994
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 625)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
            Seaton,C.L. and Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - 20-45 DAP spike cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .625
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE0870_E02_J04"
                     /clone_lib="Wheat 20-45 DAP spike cDNA library"
                     /tissue_type="Spike and seed"
                     /dev_stage="Adult plant"
                     /lab_host="E. coli SOLR"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
                     greenhouse.  Spikes at 20 DAP and seeds at 30  to 45 DAP
                     were harvested, total RNA and poly(A) RNA were prepared, a
                     cDNA  library was made, and the cDNA clones were in vivo
                     excised to give pBluescript  phagemids in the TJ Close lab
                     (Choi, Close, Fenton) at the University of  California,
                     Riverside.  Plasmid DNA preparations and DNA sequencing
                     were  performed in the OD Anderson lab (all other authors
                     )."
BASE COUNT      178 a    161 c    156 g    130 t
ORIGIN
```

```
  Query Match             2.7%;  Score 36.2;  DB 10;  Length 625;
  Best Local Similarity   50.3%;  Pred. No. 35;
  Matches   89;  Conservative    0;  Mismatches   88;  Indels    0;  Gaps    0;

Qy     152 tcaaaaaaggccaagtgctgtttgaagacaaaaagaatccgggcgtggtgtttactgcgc 211
           ||||  | ||  |   | | || || ||   ||| ||       | |||  .  || | ||
Db     252 TCAAGCATGGTGACAAGATCTTGGACGAAGCAAACAAGGTCTTCTTGGGACACACAGTGC 311

Qy     212 cggcttcaggcaaaatcgccgcgattcaccgtggcgaaaagcgcgtacttcagtcagtcg 271
             ||  ||||||| | |  |||||| |  |  | |||     |   ||  ||| ||
Db     312 AACTGGCAATCAAAATCTCTGGCATTCACTGGTGGTACAAGGTTCCAAGCCATGCAGCCG 371

Qy     272 tgattgccgttgaaggcaacgacgaaatcgagtttgaacgctacgcacctgaagcgc 328
           | |  | | ||    | || ||  |   ||    ||  |||||  |||   ||| |
Db     372 AGGTCACAGCTGGGTACTACAACTTACATGATAGAGACGGCTACAGACCCATAGCAC 428


RESULT  40
BG605187
LOCUS       BG605187                639 bp    mRNA    linear   EST 16-APR-2001
DEFINITION  WHE2328_F06_L12ZS Wheat pre-anthesis spike cDNA library Triticum
            aestivum cDNA clone WHE2328_F06_L12, mRNA sequence.
ACCESSION   BG605187
VERSION     BG605187.1  GI:13635190
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
            Seaton,C.L. and Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Pre-anthesis spike cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .639
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE2328_F06_L12"
                     /clone_lib="Wheat pre-anthesis spike cDNA library"
                     /tissue_type="Spike before anthesis"
                     /dev_stage="Adult plant"
                     /lab_host="E. coli SOLR"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
                     greenhouse.  Whole spike with awns trimmed,  white, green
                     and yellow anther were collected and total RNA, and
                     poly(A) RNA were prepared, a cDNA library was made, and
                     the cDNA  clones were in vivo excised to give pBluescript
                     phagemids in the TJ  Close lab (Choi, Close, Fenton) at
                     the University of California,  Riverside.  Plasmid DNA
                     preparations and DNA sequencing were performed  in the OD
                     Anderson lab (all other authors)."
BASE COUNT      182 a    165 c    160 g    132 t
ORIGIN


  Query Match             2.7%;  Score 36.2;  DB 10;  Length 639;
  Best Local Similarity   50.3%;  Pred. No. 35;
  Matches   89;  Conservative    0;  Mismatches   88;  Indels    0;  Gaps    0;

Qy     152 tcaaaaaaggccaagtgctgtttgaagacaaaaagaatccgggcgtggtgtttactgcgc 211
           ||||  | ||  |   | | || || ||   ||| ||       | |||    || | ||
Db     196 TCAAGCATGGTGACAAGATCTTGGACGAAGCAAACAAGGTCTTCTTGGGACACACAGTGC 255

Qy     212 cggcttcaggcaaaatcgccgcgattcaccgtggcgaaaagcgcgtacttcagtcagtcg 271
             ||  ||||||| | |  |||||| |  |  | |||     |   ||  ||| ||
Db     256 AACTGGCAATCAAAATCTCTGGCATTCACTGGTGGTACAAGGTTCCAAGCCATGCAGCCG 315

Qy     272 tgattgccgttgaaggcaacgacgaaatcgagtttgaacgctacgcacctgaagcgc 328
           | |  | | ||    | || ||  |   ||    ||  |||||  |||   ||| |
Db     316 AGGTCACAGCTGGGTACTACAACTTACATGATAGAGACGGCTACAGACCCATAGCAC 372


RESULT  41
AL556080
LOCUS       AL556080                943 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL556080 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DK010YJ05 5
            prime, mRNA sequence.
ACCESSION   AL556080
VERSION     AL556080.1  GI:12898423
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 943)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .943
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DK010YJ05"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      185 a    293 c    297 g    152 t     16 others
ORIGIN


  Query Match             2.7%;  Score 36.2;  DB 9;  Length 943;
  Best Local Similarity   59.6%;  Pred. No. 42;
  Matches   59;  Conservative    1;  Mismatches   39;  Indels    0;  Gaps    0;

Qy    1242 ggacgaagaagacctcgctttgtgcagcttcgtctgcccgggcaaatacgaatacggccc 1301
           ||  ||  ||  ||     || |   || || |   |  ||||||| || |||   |  |||
Db     345 GGCCGCCGAGGATGGGGCCTGCGGCTGCCTGCCCAACCCGGGCACATTCGAGGAGTGCCA 404

Qy    1302 gctgttgcgcaaagtgctggaaaccattgagaaggaagg 1340
             | |  | |||||| ||||    ||||| | | |||:||
Db     405 CCGGAAGTGCAAAGAGCTGTTTCCCATTCAAATGGARGG 443


RESULT  42
AV939450
LOCUS       AV939450                489 bp    mRNA    linear   EST 18-JAN-2002
DEFINITION  AV939450 K. Sato unpublished cDNA library, strain H602 adult,
```

heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah22i02 5', mRNA sequence.
ACCESSION AV939450
VERSION AV939450.1 GI:18235247
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 489)
AUTHORS Sato,K., Saisho,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES Location/Qualifiers
source 1. .489
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="bah22i02"
/clone_lib="K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 95 a 155 c 162 g 77 t
ORIGIN

Query Match 2.7%; Score 36; DB 9; Length 489;
Best Local Similarity 49.0%; Pred. No. 35;
Matches 96; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

```
Qy    908 cggtattgaacggcgcgattacacaaggcgcgcacgattatttgggacgctaccacaatc 967
          ||||  |   || |||     |     ||| ||| ||   |  |    || | | ||||
Db    172 CGGTGATCTTCGACGCCGGAAGCACGGGCACGCGCGTGCACGTCTTCCGGTTCGACAAGA 231

Qy    968 agatttccgttatcgaagaaggccgcagcaaagagctgttcggctgggttgcgccgcagc 1027
          ||||     |  |||| |  |||  |  ||  ||| | |||| |  ||| | ||||  ||
Db    232 AGATGGAGCTCGTCGACGTCGGCGACGACATCGAGGTCTTCGCCAAGGTGGAGCCGGGGC 291

Qy   1028 cggacaaatactccatcacgcgtacaaccctcggccatttcctgaaaaacaaactcttca 1087
          |  |   ||| ||      ||          || | | | | | | |  |   ||    |
Db    292 TGAGCTCGTACGCCGGACGGCCGCAGGAGGCCGCCAAGTCCATCACACCCCTGCTGGAGA 351

Qy   1088 agttcaacacagccgt 1103
          ||   || |  |||||
Db    352 AGGCTAAGAGCGCCGT 367
```

RESULT 43
AQ161443/c
LOCUS AQ161443 612 bp DNA linear GSS 09-SEP-1998
DEFINITION mgxb0007D20r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0007D20r, DNA sequence.
ACCESSION AQ161443
VERSION AQ161443.1 GI:3557844
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 612)
AUTHORS Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 258.
FEATURES Location/Qualifiers
source 1. .612
/organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0007D20r"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."
BASE COUNT 118 a 233 c 124 g 137 t
ORIGIN

Query Match 2.7%; Score 36; DB 12; Length 612;
Best Local Similarity 45.9%; Pred. No. 39;
Matches 123; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

```
Qy    138 ggaaggcgatgccgtcaaaaaaggccaagtgctgtttgaagacaaaaagaatccgggcgt 197
          ||  ||| ||| |||   | | || |  ||  |  |||||  |        |  ||| |
Db    589 GGTGGGCAATGTCGTTGTACACGGTCTGGTAGTCCTTGAACTCGGGCTTGGTGAGGGTGG 530

Qy    198 ggtgtttactgcgccggcttcaggcaaaatcgccgcgattcaccgtggcgaaaagcgcgt 257
          |    || |  | || |  |     || || | | |    | | |||| ||| ||
Db    529 CGGCGCCACCGTTCTGGGTGTACCAGTAACCGGCACCAGCAGCAGCGGCGGCAAGGGCAC 470

Qy    258 acttcagtcagtcgtgattgccgttgaaggcaacgacgaaatcgagtttgaacgctacgc 317
            |  ||| || | |||       ||||   | ||   |||       |||    |
Db    469 CGGCAATCCAGCCGAGGTTGGACGACGAGGCCTTGGCGGGCTCGGACGAAGACGAGTAGA 410

Qy    318 acctgaagcgctggcaaacttaagcggcgaagaagtgcgccgcaacctgatccaatccgg 377
          | | |  ||    |         |||||||  |  | | |  ||| || |  | ||  |||
Db    409 AGCGGCGGCCAGCGATGGTGCGGGCGGCGAGGCCGCGTGATGCAGCCGGGGCGAACGCGG 350

Qy    378 tttgtggactgcgctgcgcacccgtccg 405
          |  | |  |||    | |   | | |||
Db    349 TGCGGGTGCTGGCGCGGGACGCAGCCCG 322
```

RESULT 44
BI464724
LOCUS BI464724 779 bp mRNA linear EST 21-AUG-2001
DEFINITION 603202344F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5268155 5', mRNA sequence.
ACCESSION BI464724
VERSION BI464724.1 GI:15255367
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 779)

```
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11676  row: h  column: 12
            High quality sequence stop: 343.
FEATURES             Location/Qualifiers
     source          1. .779
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5268155"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.2 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      200 a    197 c    242 g    140 t
ORIGIN
```

```
  Query Match             2.7%;  Score 36;  DB 10;  Length 779;
  Best Local Similarity   55.6%;  Pred. No. 44;
  Matches   69;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     631 gaattcggcggcccgcatcctgccggtttgagtggcacgcacattcatttcatcgagccg 690
           |||  |    ||||| ||||||||||  ||   |   |||  || | | ||    | |
Db     211 GAACCCCCTTGCCCGAATCCTGCCGGTGGGAAGTGGCTGCAGTTTGAATCCAAACGGGCA 270

Qy     691 gtcggcgcgaataaaaccgtgtggaccatcaattatcaagatgtaattaccattggccgt 750
           |  ||| ||| | | ||||  ||||||  |      ||  |  |   |  | |  || | |
Db     271 CTTCGCGGGAAGACAGCCGTTCGGACCACCGCAGTTCCCGGGGGCTTCCCAAAGGGGCCT 330

Qy     751 ttgt 754
           ||||
Db     331 TTGT 334
```

```
RESULT  45
BI949252
LOCUS       BI949252                 574 bp    mRNA    linear   EST 19-OCT-2001
DEFINITION  HVSME10013A08f Hordeum vulgare spike EST library HVcDNA0012
            (Fusarium infected) Hordeum vulgare cDNA clone HVSME10013A08f, mRNA
            sequence.
ACCESSION   BI949252
VERSION     BI949252.1  GI:16290354
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 574)
  AUTHORS   Wing,R., Muehlbauer,G.J., Close,T.J., Kleinhofs,A., Wise,R., Heinen
            ,S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T.,
            Simmons,J., Fenton,R.D., Malatrasi,M., Choi,D.W., Oates,R. and Main
            ,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Fusarium infected Morex spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 227
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence start: 61
            High quality sequence stop: 465.
FEATURES             Location/Qualifiers
     source          1. .574
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSME10013A08f"
                     /clone_lib="Hordeum vulgare spike EST library HVcDNA0012
                     (Fusarium infected)"
                     /tissue_type="Spike"
                     /lab_host="TJC121"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Plants were grown at the University of Minnesota in
                     the GJ Muehlbauer lab; spikes were harvested and snap
                     frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
                     graminearum inoculation (Heinen). In the TJ Close lab at
                     the University of California, Riverside, total RNA was
                     prepared from each sample pool, equal quantities of all
                     eight RNA pools were combined, poly(A) RNA was purified
                     from the mixture, one primary unamplified cDNA library was
                     made, and 1 million pfu were in vivo excised to give
                     pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi
                     ). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      178 a    128 c    137 g    123 t      8 others
ORIGIN
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  Query Match             2.7%;  Score 35.8;  DB 10;  Length 574;
  Best Local Similarity   49.7%;  Pred. No. 43;
  Matches   88;  Conservative    0;  Mismatches   89;  Indels    0;  Gaps    0;

Qy     152 tcaaaaaaggccaagtgctgtttgaagacaaaaagaatccgggcgtggtgtttactgcgc 211
           ||||  | ||  |   | | || || ||   ||| ||      | |||  |  |  |
Db     214 TCAAGCACGGTGACAGGATCTTGGATGAAGCAAACAAGGTCTTCTTGGGATACAAGGGNN 273

Qy     212 cggcttcaggcaaaatcgccgcgattcaccgtggcgaaaagcgcgtacttcagtcagtcg 271
           |  |||||  ||| ||| | |  |||||| |  |  | |||     |   ||  ||| ||
Db     274 CAACTTCAATCAAGATCTCTGGCATTCACTGGTGGTACAAGGTTCCAAGCCATGCAGCCG 333

Qy     272 tgattgccgttgaaggcaacgacgaaatcgagtttgaacgctacgcacctgaagcgc 328
           | |  | | ||    | || ||  |   ||    ||  | |||  | |   ||| |
Db     334 AGCTCACAGCTGGGTACTACAACTTACATGATAGAGACGGATACAGAACCATAGCAC 390
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Job time: 17530 sec
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